



UniGene

ORGANISED VIEW OF THE TRANSCRIPTOME

[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [Popset](#) [Taxonomy](#)Search [Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)Hs#S397514 241 bases *Homo sapiens* UniGene [Hs.389988](#)

NCBI

EST, clone IMAGE:300515, 5'end[UniGene](#)[Homepage](#)[Query Tips](#)[FAQs](#)[DDD](#)[Download UniGene](#)[Related](#)[Resources](#)[HomoloGene](#)[dbEST](#)[Trace Archive](#)[BLAST](#)[CGAP](#)[MGC cDNA clones](#)**SEQUENCE INFORMATION**GenBank entry: [W07459.1](#)

Sequence length: 241 bases

Clone: IMAGE:300515

Library: Soares_fetal_lung_NbHL19W
[dbEST 415](#)**FEATURES**[switch to text mode](#)

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Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Display GenBank all to file

Range: from to Reverse complemented strand Features: SNP
 CDD MGC HPRD STS

1: W07459. Reports za97f06.r1 Soares...[gi:1281460]

LOCUS W07459 241 bp mRNA linear EST 25-APR-1996
 DEFINITION za97f06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
 IMAGE:300515 5', mRNA sequence.
 ACCESSION W07459
 VERSION W07459.1 GI:1281460
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1 (bases 1 to 241)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
 ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
 Rifkin,L., Rohlffing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
 ,R., Williamson,A., Wohldmann,P. and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: mob.REGA+ET
 High quality sequence stop: 164.
 FEATURES Location/Qualifiers
 source 1..241
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="[GDB:1245439](#)"
 /db_xref="[taxon:9606](#)"
 /clone="IMAGE:300515"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_fetal_lung_NbHL19W"
 /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."

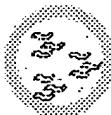
ORIGIN

```
1 tcagtttaag aatgcttaat tccttagatga actaagagtg tttattacat gttgagattt  
61 atggtatgct ttttccctt caagataatg catttttgtt attatctgtt aatgtgatag  
121 ggtaaccnat tgggaaattt ncaatcattt aacaaccctt gatTTTTTG gataaactct  
181 atnggtcat tatgcatcat tctataaacc ctgctgaant tttcatttgc caacatctta  
241 t
```

//

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Feb 5 2003 14:31:10



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SELECTED PROTEIN SIMILARITIES

Comparison of sequences in UniGene with proteins supported by a complete genome. The alignments can suggest function of a gene.

D. melanogaster	pir:S15008 - S15008 gene disco protein - fruit fly	27.74 % / 349 aa (see ProtEST)
H. sapiens	pir:A46415 - A46415 basonuclin - human	99.80 % / 993 aa (see ProtEST)
M. musculus	sp:O35914 - BASO_MOUSE Zinc finger protein basonuclin	86.84 % / 964 aa (see ProtEST)

GENE EXPRESSION

Tissues and development stages from this gene's sequences survey gene expression. Links to other NCBI expression resources.

cDNA sources: brain, colon, liver, lung, prostate, uterus, embryo, juvenile, adult

Expression Profile: View expression levels using UniGene's EST ProfileViewer

GEO profiles: Gene expression profiles in the NCBI Gene Expression Omnibus database

MAPPING POSITION

Genomic location specified by transcript mapping, radiation hybrid mapping, genetic mapping or cytogenetic mapping.

Genome View: 10

UniSTS entry: D11S4421

SEQUENCES

Sequences representing this gene; mRNAs, ESTs, and gene predictions supported by transcribed sequences.

EST Sequences (12)

CB133377.1	Clone L9SNU354-11-G07	liver	5' read
AI357412.1	Clone IMAGE:1963465	colon	3' read A
AI590539.1	Clone IMAGE:2259360	brain	3' read A
R45447.1	Clone IMAGE:35226	brain	3' read PA
AI870708.1	Clone IMAGE:2428099	uterus	3' read A
H09991.1	Clone IMAGE:46810	brain	3' read PA

BF222169.1	Clone IMAGE:3648501	prostate	3' read A
BF754676.1	Clone (no-name)	colon	
BF754824.1	Clone (no-name)	colon	
BF758462.1	Clone (no-name)	colon	
BF802655.1	Clone (no-name)	colon	
WG7459.1	Clone IMAGE:300515	lung	5' read

Key to Symbols

P Has similarity to known Proteins (after translation)
A Contains a poly-Adenylation signal
S Sequence is a Suboptimal member of this cluster
M Clone is putatively CDS-complete by MGC criteria

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There will be a pause of up to one minute before your computer receives any data. The default filename will be "download" If your operating system responds to filename suffixes, remember to choose a suffix compatible with plain text or fasta formats.



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UniSTS:76488

Links

D11S4421*Homo sapiens* chromosome 11, locus MGC16207*Pan troglodytes* chromosome 11Found by e-PCR in sequences from *Homo sapiens* and *Pan troglodytes*.

Related sites

e-PCR

Map Viewer

Gene

UniGene

dbSNP

GeneMap'99

RHdb

GDB

MGD

ZFIN

Genomic biology

Primer Information

Forward primer: TTAATCCTCAGTACATTTCAACCC

Reverse primer: TGATGCGCTACCTTGCTTC

PCR product size: 157-158 (bp), *Homo sapiens*

GenBank Accession: G06217 Z38424

Homo sapiens

Name: D11S4421

Also known as: HSC0BA112 WI-6395

Cross References

Bos taurus
Canis familiaris
Danio rerio
Homo sapiens
Mus musculus
Rattus norvegicus
Sus scrofa

Gene	GenID:	84853
	Symbol:	MGC16207
	Description:	hypothetical protein MGC16207
	Position:	11q23.3
UniGene	Hs.334846	Poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
	Hs.389988	Transcribed locus
RHdb	RH52164	
GDB	GDB:678812 G00-678-812	

Mapping Information

D11S4421	Sequence Map:	Chr 11	Map Viewer
	Position:	119036949-119037106 (bp)	

D11S4421	Sequence Map:	Chr 11 Celera	Map Viewer
	Position:	119187059-119187216 (bp)	

WI-6395	WI-RH Map:	Chr 11	Map Viewer
	Position:	546.7 (cR3000)	
	Lod score:	P0.01	

WI-6395 GM99-GB4 Map: Chr 11 Map Viewer
Position: 391.79 (cR3000)
Lod score: 0.80
Reference Interval: D11S924-D11S925 (120.8-123.5 cM)

Electronic PCR results**mRNA (5)**

BC007379.2	1211 .. 1368
BC021976.2	892 .. 1049
BC044230.2	839 .. 996
BC064140.1	836 .. 993
BC086309.1	823 .. 980

Genomic (5 of 6)[Show All Hits]

G06217.1	30 .. 187
AP003393.1	86597 .. 86754
CH003458.1	116187059 .. 116187216
CH003482.1	120411045 .. 120411202
CH003506.1	122254429 .. 122254586

Working Draft phase 1 (from GenBank HTGS division) (1)

AC036174.2	127290 .. 127447
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ESTs (5 of 72)[Show All Hits]

T10063.1	42 .. 199
Z38424.1	30 .. 187
T30207.1	35 .. 192
T85069.1	35 .. 193
T89458.1	35 .. 191

Whole Genome Shotgun sequences (3)

AADD01119913.1	12591 .. 12748
AADB01067920.1	5917 .. 6074
AADC01102571.1	11092 .. 11249

Pan troglodytes

Name: D11S4421

Mapping Information

D11S4421	Sequence Map:	Chr 11	Map Viewer
	Position:	121054383-121054539 (bp)	

Electronic PCR results



Whole Genome Shotgun sequences (2)

AADA01244170.1	3595 .. 3751
AACZ01211643.1	3611 .. 3767

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